



Figure 2

g1244708	GmANT1	1	---MKSFCDDNNHNSNTTNLGFSLSSNMMKGGRRGGREAIY-----	1	---SSSTSAAATSSSVPPQLWVGDNTSNFGCYGSNPNGG-----IYSHMNSV	85
	OsANT1	1	---MKRINESNTDDNNHNSNLGFSLSP---HMKMEA-----	1	---SHLSNFGMCYGVGENG-----FHSPLTY	71
	GhANT1	1	1 MASGNSSSSGSSMAATAGGGCGWLGFLSP---HMATCAGGVDDVG-HHHH-----	1	---SHLSNFGMCYGVGENG-----FHSPLTY	99
	GmANT2	1	1 MSNWLGFSLTP---DLRIDESEFGREDHGFP-----	1	---SHLSNFGMCYGVGENG-----FHSPLTY	30
	OsANT1	1	1 ---MKSMEENDDNADLNQNQNWLGFSLSPQMHNTGVSQSHSOPSSAEEVYPTSFYHHTAPLSSYGFYY	1	---SHLSNFGMCYGVGENG-----FHSPLTY	63
g1244708	GmANT1	41	1 ---SSSTSAAATSSSVPPQLWVGDNTSNFGCYGSNPNGG-----IYSHMNSV	41	1 ---SSSTSAAATSSSVPPQLWVGDNTSNFGCYGSNPNGG-----IYSHMNSV	85
	OsANT2	32	1 ---TSAAHTVPTTFYMSPSQ-----SHLSNFGMCYGVGENG	32	1 ---TSAAHTVPTTFYMSPSQ-----SHLSNFGMCYGVGENG	71
	GhANT1	49	1 ---HHVHQHQQQHGCGLEYN---PAQYASSFYYGGGHDAVVTSAGGGSYGGFSS	49	1 ---HHVHQHQQQHGCGLEYN---PAQYASSFYYGGGHDAVVTSAGGGSYGGFSS	99
	GmANT2	29	1 GLEAEENVGLYSALP-----D5ATTTCNFLESPPAaQMWAPSPGYYYYGGAYGDTGTTAGYYY-SHLPW	29	1 GLEAEENVGLYSALP-----D5ATTTCNFLESPPAaQMWAPSPGYYYYGGAYGDTGTTAGYYY-SHLPW	78
	OsANT1	64	1 ---AAAAGAMSSPP-----D5ATTTCNFLESPPAaQMWAPSPGYYYYGGAYGDTGTTAGYYY-SHLPW	64	1 ---AAAAGAMSSPP-----D5ATTTCNFLESPPAaQMWAPSPGYYYYGGAYGDTGTTAGYYY-SHLPW	103
g1244708	GmANT1	86	1 MPLRSQDGSLCLMEALNRS-----SHSNHHQDGS-SPKVEDOFFG---THHN-----	86	1 MPLRSQDGSLCLMEALNRS-----SHSNHHQDGS-SPKVEDOFFG---THHN-----	125
	OsANT2	72	1 MPLRSQDGSLCLMEALNRS-----QTQVMVPTG-----SPKLEDFFGATMGT-----	72	1 MPLRSQDGSLCLMEALNRS-----QTQVMVPTG-----SPKLEDFFGATMGT-----	113
	GhANT1	100	1 MPLRSQDGSLCLMEALNRS-----DQEQQGVVVG-----ASPKELEDFFG-----	100	1 MPLRSQDGSLCLMEALNRS-----DQEQQGVVVG-----ASPKELEDFFG-----	137
	GmANT2	31	1 MPLRSQDGSLCLMEALNRS-----DQEQQGVVVG-----ASPKELEDFFG-----	31	1 MPLRSQDGSLCLMEALNRS-----DQEQQGVVVG-----ASPKELEDFFG-----	98
	OsANT1	79	1 MPLRSQDGSLCLMEALNRS-----DQEQQGVVVG-----ASPKELEDFFG-----	79	1 MPLRSQDGSLCLMEALNRS-----DQEQQGVVVG-----ASPKELEDFFG-----	133
g1244708	GmANT1	104	1 MPLRSQDGSLCLMEALNRS-----DQEQQGVVVG-----ASPKELEDFFG-----	104	1 MPLRSQDGSLCLMEALNRS-----DQEQQGVVVG-----ASPKELEDFFG-----	131
	OsANT1	126	1 NTSKHEAMDLSDLSFLYN-----TTHEPNTTTTFNQEFFS-----	126	1 NTSKHEAMDLSDLSFLYN-----TTHEPNTTTTFNQEFFS-----	159
	GhANT1	114	1 HEYGSHERGLSDLSIYNSQNAEAQPNRDQLLSQPFRRQGHMNSVQ-----	114	1 HEYGSHERGLSDLSIYNSQNAEAQPNRDQLLSQPFRRQGHMNSVQ-----	158
	OsANT2	138	1 AGPAMALSLDLSIYNSQNAEAQPNRDQLLSQPFRRQGHMNSVQ-----	138	1 AGPAMALSLDLSIYNSQNAEAQPNRDQLLSQPFRRQGHMNSVQ-----	177
	GhANT1	99	1 QNTVPSPTRINVNVAAPNYSSSGD-----AEAAENFTNPSSEFTQTYRNYYENPQTLMAGG-----	99	1 QNTVPSPTRINVNVAAPNYSSSGD-----AEAAENFTNPSSEFTQTYRNYYENPQTLMAGG-----	152
	GmANT2	134	1 LSUDSvFYIQPSSRDPNNNQTY-----QNHYQHISTNQQQQQDQLQAYYSTLNRHOMILE-----	134	1 LSUDSvFYIQPSSRDPNNNQTY-----QNHYQHISTNQQQQQDQLQAYYSTLNRHOMILE-----	188
	OsANT1	132	1 CGNGSGHDPATYSSQQGEAEADASRAHYQHHQLVP-----	132	1 CGNGSGHDPATYSSQQGEAEADASRAHYQHHQLVP-----	165
g1244708	GmANT1	160	1 ---FPQTTRNHEEEETRN-YGN-----PSLTHGGSFNYGVYGEF-----QOSLSLSMSPGS-----	160	1 ---FPQTTRNHEEEETRN-YGN-----PSLTHGGSFNYGVYGEF-----QOSLSLSMSPGS-----	205
	OsANT1	159	1 HPYYSGLACHGLYQAPLEEEETTKETHVSDCSLMPQMTTEGLKNWVAPTREFSTHQQVYLEQQMNCGMGN	159	1 HPYYSGLACHGLYQAPLEEEETTKETHVSDCSLMPQMTTEGLKNWVAPTREFSTHQQVYLEQQMNCGMGN	226
	GhANT1	178	1 ---GFLQCAVTPGAGAG-----HD-----AALVHDQSAAAVAAQWAAAMHGGGYDIAANAAQDDV	178	1 ---GFLQCAVTPGAGAG-----HD-----AALVHDQSAAAVAAQWAAAMHGGGYDIAANAAQDDV	228
	GmANT2	153	1 HSLQHQCDPNPNHNQR-----SG-----VHHYPFESATSVSGFKSISLRLQTPTFPGGKASGN-----	153	1 HSLQHQCDPNPNHNQR-----SG-----VHHYPFESATSVSGFKSISLRLQTPTFPGGKASGN-----	201
	OsANT1	189	1 GSKQSQTSDNNNLLHQNMG-----GODAVPVPGLKSWEMRNFQASHAHESKMIVPHVEENAG	189	1 GSKQSQTSDNNNLLHQNMG-----GODAVPVPGLKSWEMRNFQASHAHESKMIVPHVEENAG	245
	GhANT1	166	1 YNYQPLTEAEMLQEAAAP-MEDAMAAA-----KNFLVTSYACYGNQ-EMPQQLSLSMSP	166	1 YNYQPLTEAEMLQEAAAP-MEDAMAAA-----KNFLVTSYACYGNQ-EMPQQLSLSMSP	219
g1244708	GmANT1	206	1 -QSSCITGSHHHHQNNQNHOSQNHQQI SEALVETSGFETTTLMAAAAKKKRQEDVVVGGKQKQIYHRK	206	1 -QSSCITGSHHHHQNNQNHOSQNHQQI SEALVETSGFETTTLMAAAAKKKRQEDVVVGGKQKQIYHRK	272
	OsANT2	227	2 ERNGYSLGSVGGCELQSLSMSPGSQSSCVTAPS-----GTDSYAVDAKKRSH-----AKLGKQPKWHRK	227	2 ERNGYSLGSVGGCELQSLSMSPGSQSSCVTAPS-----GTDSYAVDAKKRSH-----AKLGKQPKWHRK	287
	GhANT1	229	2 CAAGPIIPTGHLHPLTLSMSSAQSQSSCVTQAAQAGEPYMAMDAYSKKRGG-----ADRAQKQPKWHRK	229	2 CAAGPIIPTGHLHPLTLSMSSAQSQSSCVTQAAQAGEPYMAMDAYSKKRGG-----ADRAQKQPKWHRK	294
	GmANT2	202	2 ---ETNNNFFNFDQLSLTMS-----PTSRNGFPAIP-----LEWYDNKRKP-----VGKNTRESYPRK	202	2 ---ETNNNFFNFDQLSLTMS-----PTSRNGFPAIP-----LEWYDNKRKP-----VGKNTRESYPRK	252
	OsANT1	246	2 ESGSIGSMAYGDLQSLSLSMSPS-SQSSSVTSSHRASPAVVDQWMDTKKRGP-----EKVDQKQIYHRK	246	2 ESGSIGSMAYGDLQSLSLSMSPS-SQSSSVTSSHRASPAVVDQWMDTKKRGP-----EKVDQKQIYHRK	309
	GhANT1	220	2 GSQSSSSCVSAAPQQHQQQMAYAA-----GKGGCQKQPKWHRK	220	2 GSQSSSSCVSAAPQQHQQQMAYAA-----GKGGCQKQPKWHRK	280



Figure 2 continued